Polyglutamine Disease Modeling: Epitope Based Screen for Homologous Recombination using CRISPR/Cas9 System.

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Public Summary:
We have previously reported the genetic correction of Huntington's disease (HD) patient-derived induced pluripotent stem cells using traditional homologous recombination (HR) approaches. To extend this work, we have adopted a CRISPR-based genome editing approach to improve the efficiency of recombination in order to generate allelic isogenic HD models in human cells. Incorporation of a rapid antibody-based screening approach to measure recombination provides a powerful method to determine relative efficiency of genome editing for modeling polyglutamine diseases or understanding factors that modulate CRISPR/Cas9 HR.

Scientific Abstract:
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